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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=29; hr=17; min=14; sec=58; ms=546;]

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Reviewer Comments:

<110> ALBERT EINSTEIN COLLEGE OF MEDICINE OF YESHIVA UNIVERSITY
MELNICK, Ari M.
LICHT, Jonathan D.
PRIVÉ, Gilbert G.
AHMAD, Khaja Farid

Please remove the foreign accent mark from the fourth applicant's name:
foreign accent marks are non-ASCII characters, and cannot be processed.

<210> 10

<211> 17

<212> PRT

<213> Artificial

<220>

<223> consensus sequence

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> amino acid residue is Leu, Gly, or Tyr

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> amino acid residue is Val, Ile, or Arg

<220>

<221> MISC_FEATURE

<222> (3)..(3)
<223> amino acid residue is Ala, Thr, or Ser

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<223> amino acid residue is Arg or Gly

<400> 10

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro
1 5 10 15

Arg

The above <220>-<223> sections stating that the amino acids at those locations can also represent another amino acid are incorrect (e.g., for location 1, amino acid residue is Leu, Gly, or Tyr). "Leu" at location 1 can only represent itself. Please use "Xaa's" instead, and explain which amino acid residues they can represent.

Validated By CRFValidator v 1.0.3

Application No: 10582662 Version No: 1.0

Input Set:

Output Set:

Started: 2008-05-28 14:21:46.010
Finished: 2008-05-28 14:21:47.829
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 819 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 34
Actual SeqID Count: 34

| Error code | Error Description |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
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| W 213 | Artificial or Unknown found in <213> in SEQ ID (30) |

Input Set:

Output Set:

Started: 2008-05-28 14:21:46.010
Finished: 2008-05-28 14:21:47.829
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 819 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 34
Actual SeqID Count: 34

Error code Error Description

This error has occurred more than 20 times, will not be displayed

<210> 1
<211> 17
<212> PRT
<213> Homo sapiens

<400> 1

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro
1 5 10 15

Arg

<210> 2
<211> 17
<212> PRT
<213> Homo sapiens

<400> 2

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1 5 10 15

Arg

<210> 3
<211> 17
<212> PRT
<213> Homo sapiens

<400> 3

Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val Pro
1 5 10 15

Gly

<210> 4
<211> 21
<212> PRT
<213> Homo sapiens

<400> 4

Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile
1 5 10 15

Pro Arg Glu Glu Leu

<210> 5
<211> 21
<212> PRT
<213> Homo sapiens

<400> 5

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile
1 5 10 15

Pro Arg Gln Asp Ile
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<210> 6
<211> 21
<212> PRT
<213> Homo sapiens

<400> 6

Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val
1 5 10 15

Pro Gly Pro Ser Pro
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<210> 7
<211> 29
<212> PRT
<213> Homo sapiens

<400> 7

Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile
1 5 10 15

Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu Pro Leu
20 25

<210> 8
<211> 29
<212> PRT
<213> Homo sapiens

<400> 8

Asp Gly Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile
1 5 10 15

Pro Arg Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr
20 25

<210> 9
<211> 28
<212> PRT
<213> Homo sapiens

<400> 9

Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val
1 5 10 15

Pro Gly Pro Ser Pro Asn Glu Glu Asn Asn Gly Lys
20 25

<210> 10
<211> 17
<212> PRT
<213> Artificial

<220>
<223> consensus sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> amino acid residue is Leu, Gly, or Tyr

<220>
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<222> (2)..(2)
<223> amino acid residue is Val, Ile, or Arg

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<222> (3)..(3)
<223> amino acid residue is Ala, Thr, or Ser

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<221> MISC_FEATURE
<222> (4)..(4)
<223> amino acid residue is Thr or Glu

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<221> MISC_FEATURE
<222> (5)..(5)
<223> amino acid residue is Val or Ile

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<222> (6)..(6)
<223> amino acid residue is Lys or Ile

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<222> (7)..(7)
<223> amino acid residue is Glu or Ser

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<223> amino acid residue is Ala, Met, or Thr

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<222> (13)..(13)
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<223> amino acid residue is Arg or Gly

<400> 10

Leu Val Ala Thr Val Lys Glu Ala Gly Arg Ser Ile His Glu Ile Pro
1 5 10 15

Arg

<210> 11
<211> 129
<212> PRT
<213> Homo sapiens

<400> 11

Met Ala Ser Pro Ala Asp Ser Cys Ile Gln Phe Thr Arg His Ala Ser
1 5 10 15

Asp Val Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr
20 25 30

Asp Val Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr
35 40 45

Val Leu Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln
50 55 60

Leu Lys Cys Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro
65 70 75 80

Glu Gly Phe Cys Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn
85 90 95

Leu Arg Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu
100 105 110

Gln Met Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser
115 120 125

Glu

<210> 12
<211> 127
<212> PRT
<213> Artificial

<220>
<223> synthetic mutant

<400> 12

Gly Ser Ala Asp Ser Gln Ile Gln Phe Thr Arg His Ala Ser Asp Val
1 5 10 15

Leu Leu Asn Leu Asn Arg Leu Arg Ser Arg Asp Ile Leu Thr Asp Val
20 25 30

Val Ile Val Val Ser Arg Glu Gln Phe Arg Ala His Lys Thr Val Leu
35 40 45

Met Ala Cys Ser Gly Leu Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys
50 55 60

Arg Asn Leu Ser Val Ile Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly
65 70 75 80

Phe Asn Ile Leu Leu Asp Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg
85 90 95

Glu Gly Asn Ile Met Ala Val Met Ala Thr Ala Met Tyr Leu Gln Met
100 105 110

Glu His Val Val Asp Thr Cys Arg Lys Phe Ile Lys Ala Ser Glu
115 120 125

<210> 13

<211> 93

<212> DNA

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<223> oligonucleotide for plasmid construction

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agctgcggca cacgccccgag ctgccccctgg ccc 93

<210> 14

<211> 93

<212> DNA

<213> Artificial

<220>

<223> oligonucleotide for plasmid construction

<400> 14

tcgaggggcca ggggcagtc gggcgtgtgc cgcaagtcct cgcgcggat ctcatggatg 60

gagcggccccg cctccttac cgtggccacc agc 93

<210> 15
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<212> DNA
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<220>
<223> oligonucleotide for plasmid construction

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agctgcggca cacgccccgag ctgcccctgg ccc 93

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<212> DNA
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<223> oligonucleotide for plasmid construction

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tcgaggggca ggggcagctc gggcggtgtgc cgcaagctcct cagctgcagc tgcattggatg 60
gagcggcccg cctccttcac cgtggccacc agc 93

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<212> DNA
<213> Artificial

<220>
<223> primer

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catcctgggc cattaccta 20

<210> 18
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 18
tctctctctg catcttgggg 20

<210> 19
<211> 20
<212> DNA
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<220>
<223> primer

<400> 19
gactctgaag agccacacctgc 20

<210> 20
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 20
ctggcttttg tgacggaaat 20

<210> 21
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 21
ccggacctaa tccctcactc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial

<220>
<223> primer

<400> 22
cacaccgatg cagtttcta 20

<210> 23
<211> 21
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<220>
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<400> 23
aaaggaaccc cacgaagtgt t 21

<210> 24
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<212> DNA
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<220>
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<400> 24

tcaagggcat atcctacaac aa

22

<210> 25
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<220>
<223> primer

<400> 25
acgatgctgg gtcaggatc

20

<210> 26
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<220>
<223> primer

<400> 26
agtgactagg gcgcgtgtgtt

20

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<220>
<223> primer

<400> 27
gggttcttag aagtgggtat gc

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<210> 28
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<220>
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<400> 28
tgggactaat ctccggcatt

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<210> 29
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<400> 29
cgatgaggag tttcggatg t 21

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tttctgggg ctctgtggac t 21

<210> 31
<211> 25
<212> PRT
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<400> 31

Cys Ala Ile Tyr Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp
1 5 10 15

Val Val Pro Gly Pro Ser Pro Asn Glu
20 25

<210> 32
<211> 17
<212> PRT
<213> Homo sapiens

<400> 32

Arg Ser Glu Ile Ile Ser Thr Ala Pro Ala Ser Ala Val Ala Pro Gly
1 5 10 15

Pro

<210> 33
<211> 17

<212> PRT
<213> Homo sapiens

<400> 33

Arg Ser Glu Ile Ile Ser Thr Ala Pro Trp Ser Ser Val Val Pro Gly
1 5 10 15

Pro

<210> 34
<211> 17
<212> PRT
<213> Homo sapiens

<400> 34

Arg Ser Glu Ile Ile Ser Thr Ala Pro Ser Ser Trp Val Val Pro Gly
1 5 10 15

Pro